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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: January 9, 2003, 12:23:23 ; Search time 15 Seconds
(without alignments)

83.316 Million cell updates/sec
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US-09-632-429-4 89 1 WEVLCWTWETCER 13	BLOSUM62 Gapop 10.0 , Gapext 0.5
Title: Perfect score: Sequence:	Scoring table:

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_73:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	_		hypothetical prote	ŀ	hypothetical prote		superoxide dismuta	cytochrome P450 (C	cytochrome P450 -	probable cytochrom	а		hypothetical prote	urease (EC 3.5.1.5	probable calcium-a	3-dehydroshikimate	methylmalonyl-CoA	ERCC1-like excisio							hypothetical prote	unknown protein F2		ы	hypothetical prote
SUMMARIES	Ωī	S70117	B96610	T41257	T19048	T21303	S47466	A53294	T10000	T09999	T09944	D69373	T45766	E85025	875169	T09172	A22421	836808	E71621	T47351	S48776	A75316	808500	B31277	T10036	T16658	A96766	D71347	AD0014	G96814
	BB	7	7	7	7	7	7	7	7	7	~	7															7	7	7	7
	Length	292	395	427	1080	1121	1230	203	516	524	524	347	475	501	569	731	359	519	242	276	278	306	330	340	481	464	575	594	732	856
* Query	_ '	57.3	55.1	51.7	51.7	51.7	51.7	49.4	48.3	48.3	•	47.2	47.2	47.2	47.2	47.2	46.6	46.6	46.1	46.1				46.1	46.1	46.1	46.1	46.1	46.1	46.1
	Score	51	49	46	46	46	46	44	43	43	43	42	42	42	42	42	41.5	41.5	41	41	41	41	41	41	41	41	41	41	41	41
Result	NO.	г	7	e	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

hypothetical prote	nypothetical prote hypothetical prote giant protein p619	hypothetical prote	glycosyl transfera	nypounetical proce cysteine proteinas	hypothetical prote enhancer of split	hypothetical prote	denydrosmikimate u hypothetical prote	hypothetical prote
T00260 H82511	T21432 T47325 S71752	37173 A70513 S46749	D87531	T49840 G86232	T19963 B49555	T29775	JN0250	AC3330
77	900	4 77 6	10	~ ~	~ ~	7	2 0	0
951	1711	280	306	415 416	614	855	348	93
46.1 46.1	45.1	44.0	44.	44 44.9	44.9	44.9	44.4	43.8
41	40.5	4 0.4 0.4 0.0	40	4 <b>4</b> 0 <b>4</b>	40	40	39.5	9.00
30	33.5	3.5	37	8 6 8 6	40	42	43	45

## ALIGNMENTS

hypothetical protein YDR287w - yeast (Saccharomyces cerevisiae) N.Alternate names: hypothetical protein D9819.7 C.Species: Saccharomyces cerevisiae C.Date: 24-Ang-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002 C.Accession: 870117 R.Fulton, L.
C;Species: Saconaromyces cerevisiae C;Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002 C;Accession: S70117 R;Fulton, L
R;Fulton, L.
submitted to the EMBL Data Library, May 1990 A. Description: The sequence of S. cerevisiae cosmid 9819. A. Reference number: S70114
A; Accession: S70117 A; Molecule type: DNA A; Residues: 1-292 <fuls A; Cross-references: EMBL:U51031; NID:g1332635; PID:g1332637; GSPDB:GN00004; MIPS:YDR2</fuls 
C;Genetics: A;Gene: MIPS:YDR287w A;Cross-references: SGD:S0002695 A;Map position: 4R C;Superfamily: suppressor protein suhB
Query Match 57.3%; Score 51; DB 2; Length 292; Best Local Similarity 54.5%; Pred. No. 3.3; Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 1 WEVLCWTWETC 11                 Db 223 WEGGCWAWDVC 233
RESULT 2 Bypothetical protein TBL23.7 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Decession: B6610 C; Date: 02-Mar-2001 #text_change 31-Mar-2001 C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C; Date: 02-Mar-2001 #text_change 31-Mar-2001 C; Date: 02-Mar-2001 #text_change 31-Mar-2001 C; Date: 03-Mar-2001 #text_change 31-Mar-2001 C; Mature 408, 816-820, 2000 A; Huibes, B.; Huizar, L. Canway, A.R.; Creasy, T.H.; Dewar, A; Dature 408, 816-820, 2000 A; Lib, J.H.; Lib, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia C, A.; Lib, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Min D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Accession: B96610 A; Residues: Preliminary A; Molecule type: DMA A; Residues: 1-395 SSTO> A; Residues: 1-395 SSTO> A; Cross-references: GB: AE005173; NID: g11055860; PIDN: AAG28328.1; GSPDB: GN00141

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Best Local Similarity 75.0%;
Matches 6; Conservative
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EGLCYPWHICE 60
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Best Local Similarity
Matches 6; Conserv
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Matches 7; Conserv
                                                                                                        886 LLWTWQTC 893
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                                                                               4 LCWTWETC 11
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S47466
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                                                                                                                                                                                                                                                                                                                     hypothetical protein SPCC285.11 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41257
R;Seeger, K.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
R;Seeger, K.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
A;Reference number: 221981
A;Reference number: 221981
A;Accession: T41257
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T41257
A;Residues: 1-427 <SEE>
A;Reperimental source: strain 972h-; cosmid c285
C;Genetics:
A;Gene: SPDB:SPCC285.11
A;Map position: 3
A;Introns: 36/3
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A;Experimental source: clone F23B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probable Pro-X carboxypeptidase F23B2.12 - Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Cat-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 R;McMurray, A. Submitted to the EMBL Data Library, December 1995 A;Reference number: 219065 A;Reference number: 219065 A;Reference number: translated from GB/EMBL/DDBJ A;Reference prejiminary; translated from GB/EMBL/DDBJ A;References: EMBL:268295; PIDN:CAA92588.1; GSPDB:GN00022; CESP:F23B2.
                                                                                                                                          Gaps
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                                                                                             Score 49; DB 2; Length 395;
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                                                                                                                                        3; Indels
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R:McMurray, A.
Submitted to the EMBL Data Library, November 1996
A:Reference number: 219403
A:Accession: T21307
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Residues: 1-1080 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
A; Genetics:
A; Gene: CESP: F23B2.12
A; Map position: 4
A; Introns: 19/2; 127/2; 287/3; 349/1; 658/2; 916/2
C; Keywords: duplication
                                                                                                               Pred. No. 8.3;
2; Mismatches
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2; Mismatches
                                                                                        55.1%;
54.5%;
                                                                               Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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284 WKLLSWAWLTC 294
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                                        A; Map position: 1
C;Genetics:
A;Gene: T8L23.7
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Length 1080;

DB 2;

51.7%; Score 46;

Query Match

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A53294
superoxide dismutase (BC 1.15.1.1) (Mn) - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 18-Jun-1999
C;Accession: A53294; JC4981
C;Accession: A53294; JC4981
C;Accession: A53294; JC4981
C;Accession: A55294; JC599
J. Bacteriol. 175, 7658-7665, 1993
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                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November 1996
A;Reference number: 219403
A;Accession: T21303
A;Accession: T21303
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1121 <WIL>
A;Cross-references: EMBL:282266; PIDN:CAB05185.1; GSPDB:GN00022; CESP:F23B2.11
C;Genetics:
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0
                                                                                                                                                                                     hypothetical protein F23B2.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Spate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21303
R;McMurray, A.
                      Gaps
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Pred. No. 56;
1; Mismatches 1; Indels
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                      Indels
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A; Map position: 4
A; Introns: 40/2; 170/2; 330/3; 392/1; 701/2; 958/2
Pred. No. 54;
1; Mismatches
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75.0%;
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9 12:19:08

The Jan

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R;Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Wer Plant Sci. 96, 129-136, 1994
A;Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Cathara A;Reference number: 216915
A;Accession: T09999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable cytochrome P450 protein - Madagascar periwinkle
N;Alternate names: CYP72 protein
C;Species: Catharanthus roseus (Madagascar periwinkle)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C;Accession: T09944
R;Vetter, H.P.: Mangold, U.; Schroeder, G.; Marner, F.J.; Werck-Reichhart, D.; Schroe Plant Physiol. 100, 998-1007, 1992
A;Title: Molecular analysis and heterologous expression of an inducible cytochrome P-A;Reference number: 216902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenic protein (bcsp31-3) homolog - Archaeoglobus fulgidus
C;Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000
C;Accession: D6973
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
J; Flaischmann, R.D.; Quackenbush, J; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A;Reference number: A69250; MUID:98049343; PMID:9389475
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                                                                                                                                                                                               A Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-524 < MANA
A; Cross-references: EMBL:L19074; NID:g404687; PID:g404688
A; Experimental source: cv. cp3
C; Genetics:
A; Gene: CYP72B
A; Introns: 96/1; 170/3; 252/2; 381/3
A; Introns: 96/1; 170/3; 252/2; 381/3
C; Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C; Keywords: heme; iron; metalloprotein
F; 329-492/Doomain: cytochrome P450 homology < P45>
F; 470/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CYP72
C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
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F;329-492/Domain: cytochrome P450 homology <P45>
F;470/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-524 <VET>
A,Cross-references: EMBL:L10081; NID:g167483; PID:g167484
C;Genetics:
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Pred. No. 76;
1; Mismatches
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53.8%;
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Matches 7; Conservative
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nes 7; Conserv
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Matches
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D69373
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C; Species: Catharanthus roseus (Madagascar periwinkle)
C; Species: Catharanthus roseus (Madagascar periwinkle)
C; Species: 16-0ul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C; Accession: T10000
R; Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-Plant Sci. 96, 129-136, 1994
A; Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanth A; Reference number: 216915
A; Reference number: 216915
A; Reference number: 216915
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-516 <AMN>
A; Residues: 1-516 <AMN>
A; Ciossreferences: EMBL:L19075; NID:g404689; PID:g404690
A; Sexperimental source: cv. cp3
C; Genetics:
A; Genetics
                                                                                                       A Accession: A53294
A Status: preliminary
A Molecule Lype: DNA
A Cross-references: GB:L25672
A Cross-references: GB:L25672
A Cross-reference GB:L25672
A Cross-reference GB:L25672
A Molecule Lype: DNA
A Cross-reference GB:U72494; NID:968609; PIDN:AABI7391.1; PID:91628613
A Molecule Lype: DNA
A Cross-references: GB:U72494; NID:91628609; PIDN:AABI7391.1; PID:91628613
C Genetics:
A,Title: Cloning and characterization of the Pseudomonas aeruginosa sodA and sodB genes dismutase activity in alginate-producing bacteria.
A,Reference number: A53294; MUID:94064560; PMID:8244935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen C; Superfamily: superoxide dismutase (Mn)
C; Keywords: homodimer; manganese; metalloprotein; oxidoreductase
F; 27, 81, 164, 168/Binding site: manganese (His, His, Asp, His) #status predicted
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C.Species: Catharanthus roseus (Madagascar periwinkle)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C.Accession: T00999
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Pred. No. 24;
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Pred. No. 75;
1; Mismatches
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14 WRVLDWAWFTPKR
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Best Local Similarity
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C;Complex: homodimer
C;Function:
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urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)
N.Alternate names: protein s111750
N.Alternate names: protein s111750
A.Variety: PCC 6803
C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C.Accession: S75169
R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
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Matches 6; Conservative
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371 EVICRTWQTAHK 382
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Matches 6; Conserv
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                            RESULT 14
S75169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F24M12.390 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 20-Jun-2000
C;Accession: T45766
R;Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke, abuminted to the Protein Sequence Database, December 1999
A;Reference number: Z23012
A;Accession: T45766
A;Accession: Preliminary
A;Accession: Preliminary
A;Residues: 1-475 <VIT>
A;Residues: 1-475 <VIT>
A;Residues: 1-475 <VIT>
A;Residues: 1-475 <VIT>
A;Resperimental source: cultivar Columbia; BAC clone F24M12
C;Genetics:
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C. Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C. Accession: E85025
R. Ancression: E85027
R. Ancression: E85025
R. Ancression: E85001; Mulb:20083488; PMID:10617198
A. Reference and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A. Recession: E85002
                                                    A;Molecule type: DNA
A;Residues: 1-347 <KLE>
A;Cross-references: GB:AE001036; GB:AE000782; NID:g2689359; PIDN:AAB90255.1; PID:g264961
C;Superfamily: immunogenic protein BCSP31
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A;Moleoule type: DNA
A;Residues: 1-501 cSTO>
A;Cross-references: GB:NC_001268; NID:g7268583; PIDN:CAB80692.1; GSPDB:GN00140
                          A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Introns: 100/2; 147/3; 225/2; 302/2; 319/2; 356/3; 375/3; 399/1
A;Note: F24M12.390
C;Superfamily: Arabidopsis thaliana hypothetical protein F24M12.380
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47.2%; Score 42; DB 2; Length 475;
Best Local Similarity 60.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                           h Similarity 54.2%; Score 42; DB 2; Length 347; Similarity 54.5%; Pred. No. 74; 6; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                            2 EVLCWTWETCE 12
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                                                                                                                                                                                                                        Best Local Similarity
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15 VVCWGFERCE 24
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A; Accession: D69373
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T45766
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A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S75169
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross references: EMBL:D90903; GB:AB001339; NID:g1652127; PIDN:BAA17083.1; PID:g165
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: January 9, 2003, 12:25:09
Job time : 16 secs
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C;Keywords: potassium channel; schizophrenia
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